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EXAMINER	
GOLDBERG, JEANINE ANNE	

ART UNIT	PAPER NUMBER
1634	

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Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/010,749	ESCARY, JEAN-LOUIS	
	Examiner	Art Unit	
	Jeanine A Goldberg	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *three* MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 November 2003*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-27* is/are pending in the application.

4a) Of the above claim(s) *1-9,15,17-25 and 27* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *10-14,16 and 26* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. §§ 119 and 120

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

13)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application) since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

a) ☐ The translation of the foreign language provisional application has been received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121 since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____.
4) ☐ Interview Summary (PTO-413) Paper No(s). _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other:

DETAILED ACTION

1. This action is in response to the papers filed November 10, 2003. Currently, claims 1-27 are pending. Claims 1-9, 15, 17-25, 27 have been withdrawn as drawn to non-elected subject matter.

Election/Restrictions

2. Newly submitted claims 1-9, 26, 27 are directed to an invention that is independent or distinct from the invention originally claimed for the following reasons.

Newly amended claims 1-9, 27 are drawn to methods for identifying therapeutically useful compounds based on at least one functional SNP. The objective of the method and the method steps have been amended such that the final goal of the method is no longer identifying SNPs, but identifying therapeutic compounds which comprises a polypeptide, gene or a molecule capable of functionally interacting with the polypeptide or gene. It is not crystal clear how one uses the SNPs identified to identifying a therapeutically useful compound, however, the reagents, method steps and goals each differ. The newly amended claims require a new search, as suggested by applicant. Further, on page 22 of the response, Applicant's clearly set forth reasons why the references which deal with SNPs are not directly related to therapeutically useful compounds. Additionally, the applicant describes their invention by first selecting the compound of interest, and evaluating copies of the gene. This invention was not previously presented and would have been restricted had it been present. The applicant asserts that "this approach to finding the 'benefits' of nature's experimentation

via SNP induced variations differs remarkably, and unobviously, from the classical approach exemplified in the cited art (page 22-23 of response filed November 7, 2003).

Since applicant has received an action on the merits for the originally presented invention, this invention has been constructively elected by original presentation for prosecution on the merits. Accordingly, claims 1-9, 15, 17-25, 27 are withdrawn from consideration as being directed to a non-elected invention. See 37 CFR 1.142(b) and MPEP § 821.03.

Priority

3. This application claims priority to foreign filed France 0015838, filed 12/6/00.

Receipt is acknowledged of papers submitted under 35 U.S.C. 119(a)-(d), which papers have been placed of record in the file.

A translation has been received.

Drawings

4. The drawings are acceptable.

New Grounds of Rejection Necessitated by Amendment

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

5. Claims 16, 26 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A1) Claim 16 is so indefinite that a search of the claim is no longer possible. Claim 16 is a method for generating a map of genetic markers comprising the functional SNPs identified in at least one preselected gene by the method of claim 1. Claim 1 is no longer drawn to a method for identifying SNPs. Claim 1 has been amended to a method for identifying a therapeutically useful compound based upon at least one functional SNP in a gene. Thus, it is unclear how Claim 1 is performed to be used in the method of Claim 16. Claim 16 does not rely upon any detecting of therapeutically useful compounds.

B1) Claim 26 is indefinite over the recitation "whereby said therapeutic compound comprises...." Because the claim does not provide any therapeutic compound. The method is directed to identifying SNPs with the intended use of using the SNPs to develop a protein useful as an active ingredient in a medicament.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

6. Claim 26 is rejected under 35 U.S.C. 102(b) as being anticipated by Dresdale et al (PNAS, Vol. 97, No. 19, pages 10483-10488, September 12, 2000).

For the purpose of complete examination, the examiner has assumed that the whereby clause for "said therapeutic compound comprises said polypeptide..." may have been residual language from a prior claim and was not intended to be part of the instant claims, as the claim would make sense without the clause.

Drysdale et al. (herein referred to as Drysdale) teaches analyzing various combinations of SNPs to identify those with functionality. Specifically Drysdale teaches selecting the human B2-adrenergic receptor gene, providing a sample of individuals from a index repository of "apparently normal individuals", isolating the B2AR gene, identifying thirteen SNPs in the B2AR gene which were organized into 12 haplotypes; and performed an analysis of protein and mRNA expression to determine functionality. Drysdale teaches sampling "normal individuals" from a repository consisting of 23 Caucasians, 19 African Americas, 20 Asians, and 15 Hispanic Latinos (Table 1 and page 10485, col. 1, para 2). These individuals do not have any particular genotype or phenotype which is "known". Drysdale teaches using the reference sequence for the intronless human B2AR gene (Genbank Accession M15169)(page 10484, col. 1). The PCR products using genomic DNA as template were sequenced (page 10484, col. 2). Drysdale teaches identifying 8 SNPs in the 5' UTR and 5 additional SNPs, three of which alter the encoded residues in the protein (Table 1, page 10484, col. 1). The PCR products from the B2AR gene were placed in a vector and receptor expression was determined by radioligand binding, and mRNA levels were determine by using

ribonuclease protection assays (page 1484, col. 2). Dresdale states that for both protein and mRNA expression, the results of the study are entirely consistent with the in vivo findings. Dresdale concludes that "the results indicate that the unique interactions of multiple SNPs within a haplotype ultimately affect biologic and therapeutic phenotype" (page 10488, col. 2). Since, Dresdale teaches every limitation of the instant claims, Dresdale anticipates the instant claims.

Response to Arguments

The response traverses the rejection. The response asserts that Drysdale does not suggest first searching "individuals chosen substantially at random from a general population." This argument has been reviewed but is not convincing because the subjects tested by Drysdale were obtained from DNA that was derived from immortalized lymphocytes from an index repository of apparently normal individuals. These individuals do not appear to have been selected from the general world population by any other means than substantially random. The response fails to provide any guidance why this population is not individuals substantially at random from a general population without any selection criteria.

The response further argues that the protein expression and mRNA expression of Figure 3 and 4 do not permit the determination of the functionality of any SNP in the gene bur are relative to two haplotypes (page 13 of response filed). This argument has been thoroughly reviewed, but is not found persuasive because the claim is drawn to a method for identifying at least on SNP. At least one SNP encompasses a full haplotype as studied by Drysdale. The claim does not require determining the functionality of a

single SNP, thus, the arguments provided are not commensurate in scope with the claims. Thus for the reasons above and those already of record, the rejection is maintained.

7. Claim 26 is rejected under 35 U.S.C. 102(a) as being anticipated by Nandabalan et al. (WO 00/50436, August 31, 2000).

For the purpose of complete examination, the examiner has assumed that the whereby clause for "said therapeutic compound comprises said polypeptide..." may have been residual language from a prior claim and was not intended to be part of the instant claims, as the claim would make sense without the clause.

Nandabalan et al. (herein referred to as Nandabalan) teaches a method of identifying functional SNPs in a gene. Nandabalan selects a candidate gene, namely tissue necrosis factor receptor (TNFR1). Nandabalan samples a "normal population" of individuals whose genomic DNA was isolated from an Index Repository containing 150 human individuals (page 5, lines 34-36). The human individuals comprise 112 unrelated individuals from African, Asian, Caucasian and Hispanic/Latino descent (Table 1, page 6). Nandabalan teaches isolating nucleic acid from the individuals using PCR primers and identifying at least on SNP within the nucleic acid, namely 12 polymorphic sites (Table 5, page 38). Nandabalan also identifies which of the mutations change the coding sequence, thereby which SNPs are functional. Nandabalan teaches that allele-specific oligonucleotide primes may be used to detect TNFR1 gene polymorphisms (page 19). Nandabalan teaches that the effects of the

polymorphism identified on expression of TNFR1 may be investigated by preparing recombinant cells (page 15, lines 29-35). Nandabalan exemplifies amplifying various regions of the TNFR1 gene using primers (page 30). The PCR products were sequenced in both directions and analyzed for the presence of the polymorphisms (page 32-33)(limitations of Claims 4-5). Nandabalan also provides Table 4 indicating observed genotypes and haplotype pairs for TNFR1 (page 35). Figure 4 illustrates the SNPs within the coding sequence and Figure 5 illustrates the SNPs which alter the protein sequence. The SNPs which alter the protein sequence are functional to the extent that the protein sequence is altered, i.e. modifies the functionality of the preselected candidate gene (as defined in the instant specification, paragraph 93). Since, Nandabalan teaches every limitation of the instant claims, Nandabalan anticipates the instant claims.

Response to Arguments

The response traverses the rejection. The response asserts that Nandabalan does not identify mutations for the purpose of identifying new therapeutic compounds. The response argues that Nandabalan studies changing the coding sequence for the purpose of using the new targets to gain an understanding of which patients may benefit from therapeutic regimes. This argument has been reviewed but is not convincing because the text of Nandabalan provides many uses for the new molecules discovered containing at least on SNP. On page 16, Nandablan teaches that recombinant cells can be used to compare the biological activities of the different protein variants (lines 10-13). On page 16 (lines 30-35), Nandabalan teaches that the invention relates to

pharmaceutical compositions for treating disorders affected by expression or function of a novel TNFR1 isogene which may comprise a polynucleotides, an antisense oligonucleotide etc.

Further, the response argues that Nandabalan does not disclose "systematically investigating the "functionality of a SNP" in order to identify new "therapeutic compounds." This arguments has been thoroughly reviewed but not persuasive because Claim 26 is drawn to identifying at least one SNP. At least one SNP comprises an entire haplotype. Thus, Nandabalan does teach assaying for haplotypes. Regardless, Nandabalan contemplates determining whether variants of the protein have different biological activities.

The response agues that Nandabalan does not identify functional SNPs from a general population. This argument has been thoroughly reviewed, but is not found persuasive because the subjects tested by Nandabalan were obtained from DNA that was derived from immortalized lymphocytes from an index repository of apparently normal individuals. These individuals do not appear to have been selected from the general world population by any other means than substantially random. The response fails to provide any guidance why this population is not individuals substantially at random from a general population without any selection criteria.

Thus for the reasons above and those already of record, the rejection is maintained.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

8. Claims 10-11 are rejected under 35 U.S.C. 103(a) as being unpatentable over Dresdale et al (PNAS, Vol. 97, No. 19, pages 10483-10488, September 12, 2000) or Nandabalan et al. (WO 00/50436, August 31, 2000) in view of Apffel et al. (US Pat. 6,379,889, April 30, 2002).

Drysdale et al. (herein referred to as Drysdale) teaches analyzing various combinations of SNPs to identify those with functionality. Specifically Drysdale teaches selecting the human B2-adrenergic receptor gene, providing a sample of individuals from a index repository of "apparently normal individuals", isolating the B2AR gene, identifying thirteen SNPs in the B2AR gene which were organized into 12 haplotypes; and analysis of protein or mRNA expression to determine functionality. Drysdale teaches sampling "normal individuals" from a repository consisting of 23 Caucasians, 19 African Americas, 20 Asians, and 15 Hispanic Latinos (Table 1 and page 10485, col. 1, para 2). These individuals do not have any particular genotype or phenotype which is "known" (limitations of Claim 3). Drysdale teaches using the reference sequence for the intronless human B2AR gene (Genbank Accession M15169)(page 10484, col. 1). The PCR products using genomic DNA as template were sequenced (page 10484, col. 2)(limitations of Claim 5). Drysdale teaches identifying 8 SNPs in the 5' UTR and 5

additional SNPs, three of which alter the encoded residues in the protein (Table 1, page 10484, col. 1)(limitations of Claim 16). The PCR products from the B2AR gene were placed in a vector and receptor expression was determined by radioligand binding, and mRNA levels were determine by using ribonuclease protection assays (page 1484, col. 2)(limitations of Claim 4, 8-9). Dresdale states that for both protein and mRNA expression, the results of the study are entirely consistent with the in vivo findings. Dresdale concludes that "the results indicate that the unique interactions of multiple SNPs within a haplotype ultimately affect biologic and therapeutic phenotype" (page 10488, col. 2).

Nandabalan et al. (herein referred to as Nandabalan) teaches a method of identifying functional SNPs in a gene. Nandabalan selects a candidate gene, namely tissue necrosis factor receptor (TNFR1). Nandabalan samples a "normal population" of individuals whose genomic DNA was isolated from an Index Repository containing 150 human individuals (page 5, lines 34-36). The human individuals comprise 112 unrelated individuals from African, Asian, Caucasian and Hispanic/Latino descent (Table 1, page 6)(limitations of Claim 2-3). Nandabalan teaches isolating nucleic acid from the individuals using PCR primers and identifying at least on SNP within the nucleic acid, namely 12 polymorphic sites (Table 5, page 38). Nandabalan also identifies which of the mutations change the coding sequence, thereby which SNPs are functional. Nandabalan teaches that allele-specific oligonucleotide primes may be used to detect TNFR1 gene polymorphisms (page 19). Nandabalan teaches that the effects of the polymorphism identified on expression of TNFR1 may be investigated by

preparing recombinant cells (page 15, lines 29-35). Nandabalan exemplifies amplifying various regions of the TNFR1 gene using primers (page 30). The PCR products were sequenced in both directions and analyzed for the presence of the polymorphisms (page 32-33)(limitations of Claims 4-5). Nandabalan also provides Table 4 indicating observed genotypes and haplotype pairs for TNFR1 (page 35). Figure 4 illustrates the SNPs within the coding sequence and Figure 5 illustrates the SNPs which alter the protein sequence (limitations of Claim 8, 16). The SNPs which alter the protein sequence are functional to the extent that the protein sequence is altered, i.e. modifies the functionality of the preselected candidate gene (as defined in the instant specification, paragraph 93).

Gu teaches a method of determining at least on functional SNP in a gene by selecting a candidate gene, namely P2X7 receptor, sampling a "normal population", isolating nucleic acid from the individuals, identifying at least on SNP and identifying functional SNPs. Gu teaches studying P2X7 by sequencing DNA coding for the carboxyl terminal tail of P2X7. Peripheral blood lymphocytes and monocytes were obtained from 45 normal subjects (page 6)(limitations of Claim 3). Genomic DNA was extracted using a primer pair and amplified (page 7). The amplified PCR products were sequenced using electrophoresis (page 7)(limitations of Claims 4-5). A nucleotide substitution (A1513C) was found which cause a substitution for glutamic acid to alanine at amino acid position 496 (abstract, page 2). Gu teaches performing site directed mutagenesis to introduce a mutant (page 8). The functionality of the two sequences were analyzed (page 9). The function of the P2X7 receptors expressed on lymphocytes

and monocytes was compared with the genotype at position 1513 of the P2X7 gene (page 10)(limitations of Claims 8-9). Cells transfected with germline and A1513C mutation were analyzed for surface expression by quantitating binding of FITC-conjugated mAb and the ATP-induced uptake of ethidium (page 11). Gu concludes that the "data in this study shows that the function of the human P2X7 receptor is affected by the single nucleotide mutation of adenine to cytosine at position 1513 of cDNA which changes glutamic acid to alanine at amino acid position 496" (page 13). The analysis demonstrated that homozygosity (C/C) for this polymorphic mutation let to almost complete loss of P2X7 function in leukocytes while herterozygosity (A/C) gave a function which was half that of cells with the germline P2X7 sequence (page 13).

Neither Dresdale, Nandabalan, nor Gu specifically teaches identifying a SNP using multiplexing method using denaturing high performance liquid chromatography (DHPLC).

However, Apffel et al. (herein referred to as Apffel) teaches a multiplexing method for identifying nucleic acids using denaturing liquid chromatography. Apffel teaches denaturing high performance liquid chromatography for separating heteroduplex and homoduplex nucleic acid sample in a mixture is described. The method of Apfell is directed to forming hybrid mixtures from more than one individual, conducting DHPLC to compare the fragments by elution (forming one or more homogeneous groups comprising at least one mixture analyzed (col. 14-16)(limitations of Claims 6, 10). Apfell teaches that the multiplexed denaturing liquid chromatography method is a rapid method for identifying nucleic acids, specifically for distinguishing

individual polymorphic nucleic acid molecules, involves relatively fewer steps and generates information relatively quickly (col. 3, lines 37-50). The ability to multiplex allows more samples to be analyzed in the same amount of time, increasing effective sample throughput and addresses the problem of the low throughput of liquid chromatography, particularly DHPLC (col. 7, lines 27-30; col. 7, lines 36-39). Apffel teaches the method involves spectral multiplexing. Apffel teaches that the method may be used in haplotying analysis (col. 14-15).

Therefore, it would have been prima facie obvious to one of ordinary skill at the time the invention was made to have modified the SNP detection means taught in Dresdale, Nandabalan with the improved method of detecting multiple SNPs of Apffel. The ordinary artisan would have been motivated to have modified and improved the method of Dresdale, or Nandabalan by using the multiplexing method for identifying nucleic acids using denaturing liquid chromatography taught by Apffel. Apffel teaches the multiplexing method is a rapid method for identifying nucleic acids, specifically for distinguishing individual polymorphic nucleic acid molecules, involves relatively fewer steps and generates information relatively quickly (col. 3, lines 37-50). The ordinary artisan would have been motivated to be able to perform the analysis of the multiple individuals at multiple SNP sites quickly, to save time and reagents. Therefore, using the multiplexing method of Apffel to identify a functional group of SNPs, as taught by Dresdale or Nandabalan, would have been obvious to the ordinary artisan at the time the invention was made.

Response to Arguments

The response traverses the rejection. The response asserts that Drysdale and Nandabalan have been previously addressed and Apffel merely described the methods of Claim 6 and do not affect the rejection. This argument has been reviewed but is not convincing for the reasons presented above for Drysdale and Nandabalan.

In response to applicant's argument that the examiner's conclusion of obviousness is based upon improper hindsight reasoning, it must be recognized that any judgment on obviousness is in a sense necessarily a reconstruction based upon hindsight reasoning. But so long as it takes into account only knowledge which was within the level of ordinary skill at the time the claimed invention was made, and does not include knowledge gleaned only from the applicant's disclosure, such a reconstruction is proper. See *In re McLaughlin*, 443 F.2d 1392, 170 USPQ 209 (CCPA 1971). The rejection above, states, " Apffel teaches the multiplexing method is a rapid method for identifying nucleic acids, specifically for distinguishing individual polymorphic nucleic acid molecules, involves relatively fewer steps and generates information relatively quickly (col. 3, lines 37-50). The ordinary artisan would have been motivated to be able to perform the analysis of the multiple individuals at multiple SNP sites quickly, to save time and reagents" to support the combination of the references. Thus, it is not applicant's own work that the examiner relied upon, but rather the beneficial teachings of Apffel, as permitted by the law.

Thus for the reasons above and those already of record, the rejection is maintained.

9. Claims 12-14 are rejected under 35 U.S.C. 103(a) as being unpatentable over Dresdale et al (PNAS, Vol. 97, No. 19, pages 10483-10488, September 12, 2000) or Nandabalan et al. (WO 00/50436, August 31, 2000) in view of Apffel et al. (US Pat. 6,379,889, April 30, 2002) as applied to Claims 10-11 above, and further in view of Oefner et al (US Pat. 5,795,976, August 18, 1998)

Neither Dresdale, Nandabalan nor Apffel specifically teach a method of identifying SNPs using DHPLC followed by sequencing or minisequencing.

However, Oefner et al. (herein referred to as Oefner) teaches a method of performing DHPLC to identify sequence variations followed by allele specific PCR (minisequencing) to confirm the sequence. Oefner teaches that polymorphic site identification was confirmed by subsequence conventional sequencing techniques (col. 34, lines 35-43).

Therefore, it would have been prima facie obvious to one of ordinary skill at the time the invention was made to have performed DHPLC to detect SNPs, as taught by Dresdal, Nadabalan, and Apffel followed by sequencing as taught by Oefner. The ordinary artisan would have recognized that while the DHPLC method, which relies upon elution, is efficient and rapid, the elution mixture may contain additional sequences in the specific elutes. Therefore, in order to confirm the results obtained by DHPLC, the ordinary artisan would have recognized that performing a sequencing reaction to confirm the results would have provided additional certainty for the identity of the sequence, as taught by Oefner. The ordinary artisan would have desired additional confidence and certainty to the results of the experiment and would have performed

additional methods to confirm the identity of the sequence. Therefore, it would have been prima facie obvious to one of ordinary skill at the time the invention was made to confirmed the polymorphic site identification using conventional sequencing techniques as specifically taught by Oefner.

Response to Arguments

The response traverses the rejection. The response asserts that the rejection is improper for the reasons discussed previously. This argument has been reviewed but is not convincing for the reasons discussed above.

It is noted that the newly amended claims directed to identifying therapeutics have been withdrawn from consideration as non-elected by original presentation. The response acknowledges that methods for detecting SNPs and method of identifying new therapeutically useful compounds are different, as they argue that the references deal with SNPs, but not identifying therapeutically useful compounds. Thus, a restriction between identifying SNPs and therapeutically useful compounds is proper, as set forth above. Thus for the reasons above and those already of record, the rejection is maintained.

Conclusion

10. No claims allowable over the art.

11. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP

§ 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

12. Any inquiry concerning this communication or earlier communications from the examiner should be directed to examiner Jeanine Goldberg whose telephone number is (703) 306-5817. The examiner can normally be reached Monday-Friday from 8:00 a.m. to 5:30 p.m.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones, can be reached on (703) 308-1152. The fax number for this Group is (703) 305- 3014.

Any inquiry of a general nature should be directed to the Group receptionist whose telephone number is (703) 308-0196.

J. Goldberg

Jeanine Goldberg
Patent Examiner
January 28, 2004

BJ FORMAN, PH.D.
PRIMARY EXAMINER